



# EasyABC

performing efficient approximate Bayesian computation sampling schemes using 


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## Context

- A number of efficient ABC schemes have been developed (Marin *et al.* 2012, Lenormand *et al.* 2012)
- Available ABC tools: ABCtoolbox (Wegmann *et al.* 2010), ABC-SysBio (Liepe *et al.* 2010) but they have not benefited from recent improvements
- The community of  users has grown tremendously
- To better keep track of on-going improvements, a collaborative toolbox seems advantageous.

## Objectives

- Diffusing recent improvements in sequential ABC methodologies: 4 sequential schemes, 3 MCMC schemes.
- Using the  platform to ease diffusion, ergonomics and collaborative improvements.
- Easy to pipeline with the package « abc » (Csilléry *et al.* 2012)
- Making use of multicore computing

## The package EasyABC: how to use it?

### • Design a simulation code in R or a binary code

function arguments = model parameters

function values = an array of summary statistics

### • Use the built-in ABC schemes

```
# defining the model
```

```
> toy_model<-function(x){2 * x + 1 + rnorm(1)}
```

```
# defining the prior distribution
```

```
> toy_prior=list(c("unif",0,10))
```

```
# defining the target summary statistics
```

```
> sum_stat_obs=5
```

```
# defining the sequence of tolerance levels
```

```
> tolerance=c(1,0.1,0.01)
```

```
# performing a sequential ABC scheme
```

```
> post<-ABC_sequential(method="Beaumont",
```

```
model=toy_model, prior=toy_prior,nb_simul=100,
```

```
summary_stat_target=sum_stat_obs,
```

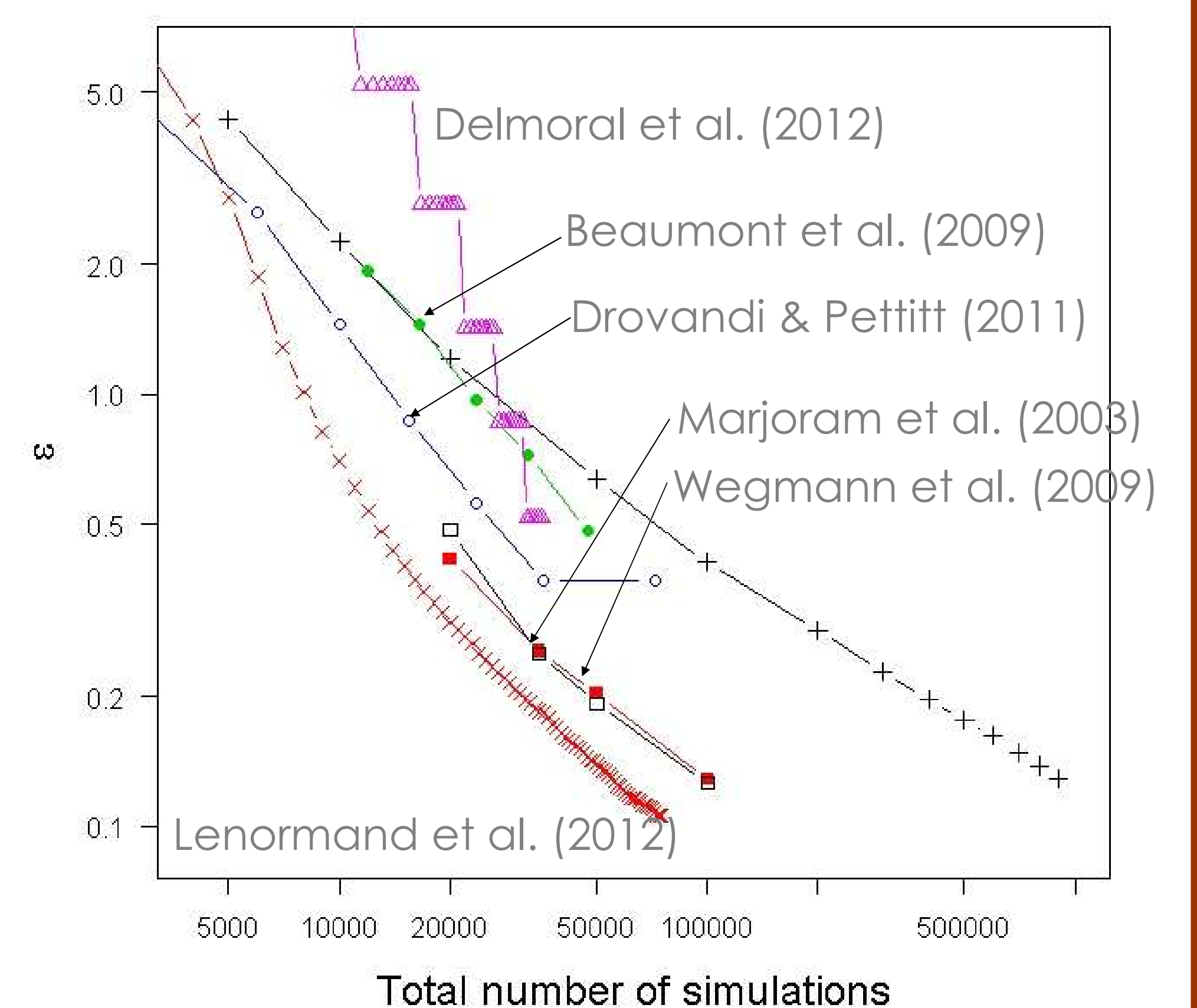
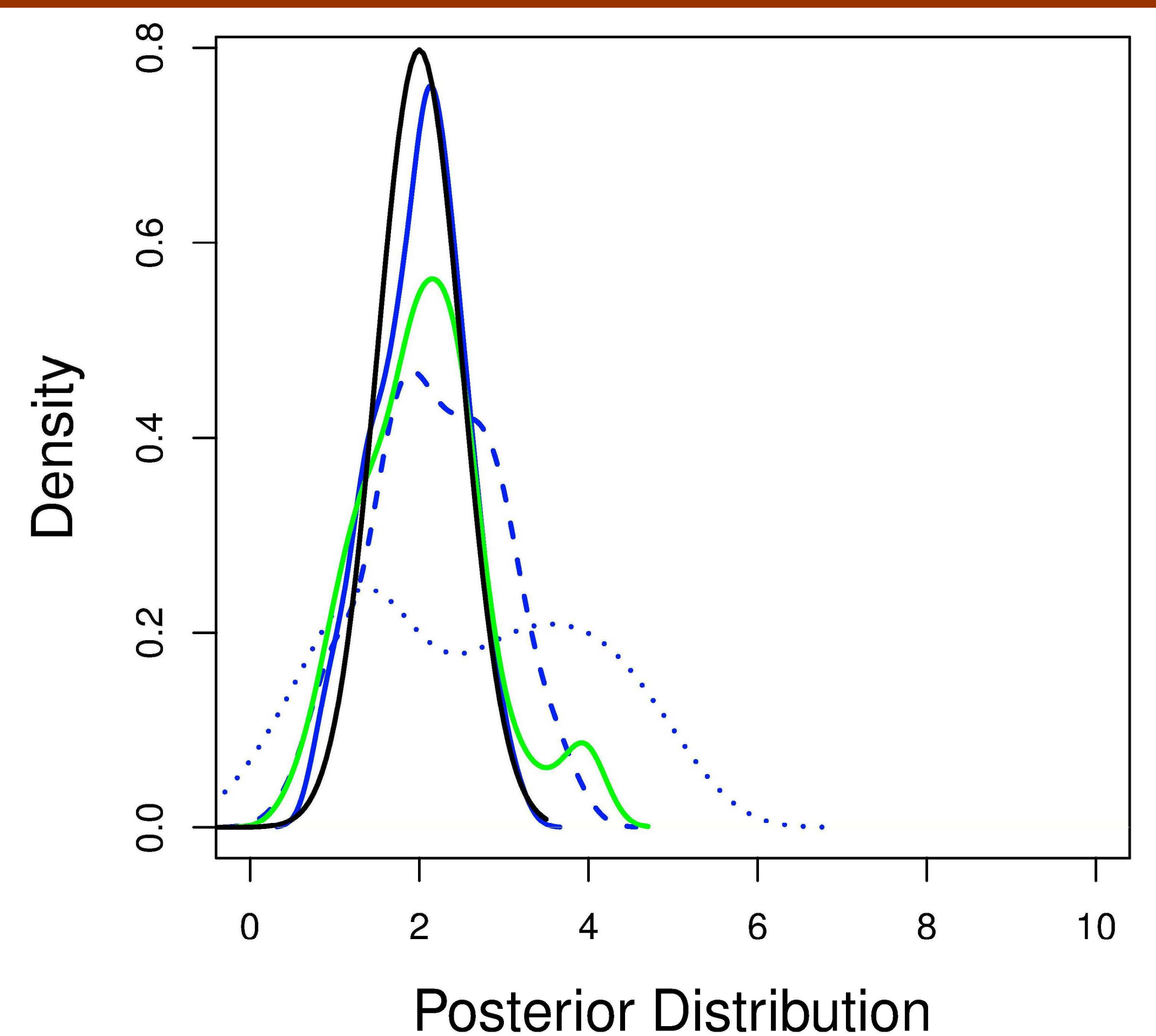
```
tolerance_tab=tolerance)
```

```
# plotting the results
```

```
> d=density(post$param,weights=post$weights)
```

```
> plot(d,type="l",col="blue")
```

**ALL CONTRIBUTIONS / SUGGESTIONS ARE WELCOME !**



## References

Csilléry, François & Blum (2012) *Methods in Ecology & Evolution*, 3, 475-479.

Jabot, Faure & Dumoulin (2013) *Methods in Ecology & Evolution*, *Online Early*.

Lenormand, Jabot & Deffuant (2012) Available on ArXiv: <http://arxiv.org/pdf/1111.1308.pdf>.

Liepe *et al.* (2010) *Bioinformatics*, 26, 1797-1799.

Marin *et al.* (2012) *Statistics and Computing*, 22, 1167-1180.

Wegmann *et al.* (2010) *BMC Bioinformatics*, 11, 116.